Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-104 (Canceled)

105. (New) A peptide probe comprising an amino acid sequence corresponding to a β-sheet forming region of a target protein, wherein the peptide probe exhibits a random coil or alpha-helix conformation in solution, and undergoes a transition to a β-sheet conformation upon interaction with misfolded target protein exhibiting a β-sheet conformation.

106. (New) The peptide probe of claim 105, wherein the peptide probe comprises at least 10 amino acid residues.

107. (New) The peptide probe of claim 105, wherein the peptide probe comprises 50 or fewer amino acid residues.

108. (New) The peptide probe of claim 105, wherein the amino acid sequence corresponding to a β-sheet forming region of the target protein is at least about 40%, at least about 70%, at least about 90% or 100% identical to the β-sheet forming region of the target protein.

109. (New) The peptide probe of claim 105, wherein the target protein is associated with a condition selected from amyloidogenic disease, Alzheimer's Disease, Prion disease, Creutzfeld Jakob disease, Gerstmann-Straussler-Scheinker Syndrome, chronic wasting disease, scrapie, bovine spongiform encephalopathy, kuru, fatal familial insomnia, transmissible spongiform encephalopathies, ALS, Pick's disease, Parkinson's disease, Frontotemporal dementia, Diabetes Type II, Multiple myeloma-plasma cell dyscrasias, Familial amyloidotic polyneuropathy, Medullary carcinoma of thyroid, Chronic renal failure, Congestive heart failure, Senile cardiac and systemic amyloidosis, Chronic inflammation, Atherosclerosis, Familial amyloidosis, and Huntington's disease.

110. (New) The peptide probe of claim 105, wherein the target protein is selected from the group consisting of APP, Aβ peptide, αl-antichymotrypsin, tau, non-Aβ component, presenilin 1, presenilin 2 apoe, prion protein, SOD, neurofilament, Pickbody, α-synuclein , amylin, IgGL-chain, transthyretin, procalcitonin); β_2-microglobulin, atrial natriuretic factor, serum amyloid A, ApoA1, gelsolin, Huntingtin, low-density lipoprotein receptor, cystic fibrosis transmembrane regulator, insulin-related amyloid, hemoglobin, rhodopsin, crystallins, p53, wildtype human TSE, human lung surfactant protein, cystatin C, and human islet amyloid polypeptide.

111. (New) The peptide probe of claim 105, wherein the peptide probe comprises an amino acid sequence that is at least about 40%, at least about 70%, at least about 90%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs 1-29.

112. (New) The peptide probe of claim 105, comprising

(a) a first amino acid sequence corresponding to a β-sheet forming region of the target protein and

(b) a second amino acid sequence corresponding to a β-sheet forming region of the target protein,

wherein the first and second amino acid sequences are the same or different and correspond to the same or different β-sheet forming regions of the target protein.

113. (New) The peptide probe of claim 112, wherein the peptide probe comprises:

(a) a first amino acid sequence corresponding to a β-sheet forming region of the target protein oriented in the forward direction, and

(b) a second amino acid sequence corresponding to a β-sheet forming region of the target protein oriented in the reverse direction.

114. (New) The peptide probe of claim 113, wherein either (i) the second amino acid sequence oriented in the reverse direction comprises the same amino sequence, in the reverse direction, as the first amino acid sequence oriented in the forward direction, or (ii) the first amino acid sequence oriented in the forward direction comprises the same amino

sequence, in the reverse direction, as the second amino acid sequence oriented in the reverse direction.

115. (New) The peptide probe of claim 112, wherein at least one of the first or second amino acid sequences comprises from 10 to 12 amino acid residues.

116. (New) The peptide probe of claim 112, further comprising a peptide linker linking the first and second amino acid sequences.

117. (New) The peptide probe of claim 116, wherein the peptide linker comprises between 1 and 10 amino acid residues.

118. (New) The peptide probe of claim 116, wherein the peptide linker comprises proline.

119. (New) The peptide probe of claim 105, labeled with a detectable label.

120. (New) The peptide probe of claim 119, wherein the detectable label is selected from (i) optically detectable moieties and (ii) radionuclides.

121. (New) The peptide probe of claim 119, wherein the detectable label is a chromophore.

122. (New) The peptide probe of claim 119, wherein the detectable label is selected from pyrene, tryoptophan, fluorescein, or rhodamine.

123. (New) The peptide probe of claim 119, wherein both termini of the peptide probe are labeled with a fluorophore capable of participating in excimer formation.

124. (New) A composition comprising a peptide probe of claim 105 bound to a misfolded target protein.

125. (New) A method for detecting misfolded target protein in a sample comprising:

(a) contacting a sample with a peptide probe according to claim 105 and permitting the peptide probe to interact with any misfolded target protein present in the sample; and

(b) detecting any interaction between the peptide probe and any misfolded target protein present in the sample.

126. (New) The method of claim 125, wherein the peptide probe is labeled with a detectable label.

127. (New) The method of claim 125, wherein (i) both termini of the peptide probe are labeled with a fluorophore and (ii) the detecting step comprises detecting any excimers formed upon interaction between the fluorophore-labeled peptide probe and any target protein present in the sample.

128. (New) The method of claim 125, wherein the detecting step comprises using circular dichroism to detect any interaction between the peptide probe and any target protein present in the sample.

129. (New) The method of claim 125, further comprising, prior to the contacting step, subjecting the sample to a disaggregation step.

130. (New) The method of claim 125, wherein the sample is a biological sample.

131. (New) The method of claim 125, wherein the sample is selected from the group consisting of tissue, meat, a biopsy sample, blood, a blood fraction, plasma, serum, pharmaceutical formulations that might contain products of animal origin, spinal fluid, saliva, urine, bodily fluids, food products, and medical products.

132. (New) The method of claim 125, wherein the target protein is associated with a condition selected from amyloidogenic disease, Alzheimer's Disease, Prion disease, Creutzfeld Jakob disease, Gerstmann-Straussler-Scheinker Syndrome, chronic wasting

disease, scrapie, bovine spongiform encephalopathy, kuru, fatal familial insomnia, transmissible spongiform encephalopathies, ALS, Pick's disease, Parkinson's disease, Frontotemporal dementia, Diabetes Type II, Multiple myeloma-plasma cell dyscrasias, Familial amyloidotic polyneuropathy, Medullary carcinoma of thyroid, Chronic renal failure, Congestive heart failure, Senile cardiac and systemic amyloidosis, Chronic inflammation, Atherosclerosis, Familial amyloidosis, and Huntington's disease.

133. (New) The method of claim 125, wherein the target protein is selected from the group consisting of APP, Aβ peptide, α1-antichymotrypsin, tau, non-Aβ component, presenilin 1, presenilin 2 apoe, prion protein, SOD, neurofilament, Pickbody, α-synuclein , amylin, IgGL-chain, transthyretin, procalcitonin); β_2-microglobulin, atrial natriuretic factor, serum amyloid A, ApoA1, gelsolin, Huntingtin, low-density lipoprotein receptor, cystic fibrosis transmembrane regulator, insulin-related amyloid, hemoglobin, rhodopsin, crystallins, p53, wildtype human TSE, human lung surfactant protein, cystatin C, and human islet amyloid polypeptide.

134. (New) The method of claim 125, wherein the peptide probe comprises an amino acid sequence that is at least about 40%, at least about 70%, at least about 90%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs 1-29.

135. (New) A method of diagnosing whether a subject suffers from, or is predisposed to, a disease associated with a misfolded target protein, comprising:

(a) obtaining a sample from the subject;

(b) contacting the sample with a peptide probe according to claim 105; and

(c) detecting interaction between the peptide probe and any misfolded target protein in the sample to assess the level of misfolded target protein present,

wherein the level of detectable misfolded target protein correlates with a diagnosis that the subject suffers from, or is predisposed to, a disease associated with the misfolded target protein.

136. (New) The method of claim 135, wherein the peptide probe is labeled with a detectable label.

137. (New) The method of claim 135, wherein (i) both termini of the peptide probe are labeled with a fluorophore and (ii) the detecting step comprises detecting any excimers formed upon interaction between the fluorophore-labeled peptide probe and any target protein present in the sample.

138. (New) The method of claim 135, wherein the detecting step comprises using circular dichroism to detect any interaction between the peptide probe and any target protein present in the sample.

139. (New) The method of claim 135, further comprising, prior to the contacting step, subjecting the sample to a disaggregation step.

140. (New) The method of claim 135, wherein the sample is a biological sample.

141. (New) The method of claim 135, wherein the sample is selected from the group consisting of tissue, meat, a biopsy sample, blood, a blood fraction, plasma, serum, pharmaceutical formulations that might contain products of animal origin, spinal fluid, saliva, urine, bodily fluids, food products, and medical products.

142. (New) The method of claim 135, wherein the target protein is associated with a condition selected from amyloidogenic disease, Alzheimer's Disease, Prion disease, Creutzfeld Jakob disease, Gerstmann-Straussler-Scheinker Syndrome, chronic wasting disease, scrapie, bovine spongiform encephalopathy, kuru, fatal familial insomnia, transmissible spongiform encephalopathies, ALS, Pick's disease, Parkinson's disease, Frontotemporal dementia, Diabetes Type II, Multiple myeloma-plasma cell dyscrasias, Familial amyloidotic polyneuropathy, Medullary carcinoma of thyroid, Chronic renal failure, Congestive heart failure, Senile cardiac and systemic amyloidosis, Chronic inflammation, Atherosclerosis, Familial amyloidosis, and Huntington's disease.

143. (New) The method of claim 135, wherein the target protein is selected from the group consisting of APP, Aβ peptide, α1-antichymotrypsin, tau, non-Aβ component, presenilin 1, presenilin 2 apoe, prion protein, SOD, neurofilament, Pickbody, α-synuclein , amylin, IgGL-chain, transthyretin, procalcitonin); β_2-microglobulin, atrial natriuretic factor, serum amyloid A, ApoA1, gelsolin, Huntingtin, low-density lipoprotein receptor, cystic fibrosis transmembrane regulator, insulin-related amyloid, hemoglobin, rhodopsin, crystallins, p53, wildtype human TSE, human lung surfactant protein, cystatin C, and human islet amyloid polypeptide.

144. (New) The method of claim 135, wherein the peptide probe comprises an amino acid sequence that is at least about 40%, at least about 70%, at least about 90%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs 1-29.

145. (New) A kit for detecting the presence of misfolded target protein in a sample comprising a peptide probe of claim 105 together with instructions for use.